

Record Date Completed: 20031110

? ds

Set	Items	Description
S1	3643	SARS OR HSARS OR SCOV
S2	270156	POLYMERASE
S3	309	S1 AND S2
S4	70	S3 NOT (PCR OR REVERSE)
S5	2455	REPLICASE
S6	50	S1 AND S5
S7	1236	ORF1 OR ORF1A OR ORF1AB
S8	7	S1 AND S7
S9	76283	ANTIBODY AND RESPONSE
S10	51	S1 AND S9
S11	8032	POL
S12	11	S10 AND (S11 OR S2 OR S5 OR S7)

? log hold

06mar06 12:29:18 User208669 Session D2995.2

\$9.87 2.903 DialUnits File155

\$0.00 148 Type(s) in Format 6

\$2.42 11 Type(s) in Format 7

\$2.42 159 Types

\$12.29 Estimated cost File155

\$3.73 TELNET

\$16.02 Estimated cost this search

\$16.44 Estimated total session cost 3.024 DialUnits

Logoff: level 05.10.03 D 12:29:18

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 17:03:25 ; Search time 78.378 Seconds  
(without alignments)  
438.412 Million cell updates/sec

Title: US-10-848-737-4  
Perfect score: 21  
Sequence: 1 gcacuugucuaccuugaugtt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Issued Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%										
Result		Query										
No.	Score	Match	Length	DB	ID	Description						
c	1	17.4	82.9	393	3	US-09-404-879A-374	Sequence 374, App					
c	2	17.4	82.9	393	4	US-09-667-857-374	Sequence 374, App					
c	3	17.4	82.9	1463	4	US-09-949-016-2910	Sequence 2910, Ap					
c	4	17.4	82.9	1520	4	US-09-919-039-342	Sequence 342, App					
c	5	17.4	82.9	1538	4	US-09-976-594-52	Sequence 52, Appl					
c	6	17.4	82.9	1542	4	US-09-919-039-341	Sequence 341, App					
c	7	17.4	82.9	1990	4	US-09-976-594-53	Sequence 53, Appl					
c	8	17	81.0	74730	4	US-09-949-016-15189	Sequence 15189, A					
c	9	16.8	80.0	924	4	US-09-248-796A-844	Sequence 844, App					
	10	16.8	80.0	1099	4	US-08-956-171E-825	Sequence 825, App					
	11	16.8	80.0	1099	4	US-08-781-986A-825	Sequence 825, App					

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 17:34:20 ; Search time 428.102 Seconds  
(without alignments)  
311.209 Million cell updates/sec

Title: US-10-848-737-4  
Perfect score: 21  
Sequence: 1 gcacuugucuaccuugaugtt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues

Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications\_NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 16:07:29 ; Search time 271.346 Seconds  
(without alignments)  
458.140 Million cell updates/sec

Title: US-10-848-737-4  
Perfect score: 21  
Sequence: 1 gcacuugucuaccuugauggt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	19	90.5	29751	12	ADJ39000	Adj39000 SARS coro
	2	17.8	84.8	237961	6	ABQ80552	Abq80552 Human Can
c	3	17.4	82.9	355	10	ACD93215	Acd93215 Human col
c	4	17.4	82.9	393	3	AAA70063	Aaa70063 Human ova

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 16:07:59 ; Search time 496.063 Seconds  
(without alignments)  
2051.271 Million cell updates/sec

Title: US-10-848-737-4  
Perfect score: 21  
Sequence: 1 gcacuugucuaccuugaugtt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
1	19	90.5	1706	14	AY322205S1	AY322205 SARS coro	
2	19	90.5	6200	14	AY534762S1	AY534762 SARS coro	
3	19	90.5	14011	14	AY534758S1	AY534758 SARS coro	

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 23:08:06 ; Search time 728.716 Seconds  
(without alignments)  
1396.372 Million cell updates/sec

Title: US-10-848-737-4  
Perfect score: 21  
Sequence: 1 gcacuugucuaccuugaugtt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	19	90.5	1706	14	AY322205S1	AY322205 SARS coro	
2	19	90.5	6200	14	AY534762S1	AY534762 SARS coro	
3	19	90.5	14011	14	AY534758S1	AY534758 SARS coro	

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 16:45:00 ; Search time 2427.07 Seconds  
(without alignments)  
329.347 Million cell updates/sec

Title: US-10-848-737-4  
Perfect score: 21  
Sequence: 1 gcacuugucuaccuugaugtt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			Description
Result	No.	Score	Match	Length	DB	ID	
	1	19	90.5	449	2	BE938410	BE938410 RC0-TN007
c	2	18.4	87.6	1076	4	BM459897	BM459897 AGENCOURT
c	3	18.4	87.6	1128	4	BG110924	BG110924 602284573
c	4	18	85.7	587	5	BP284256	BP284256 BP284256
c	5	17.8	84.8	342	9	CE508857	CE508857 tigr-gss-
c	6	17.8	84.8	600	2	BF356298	BF356298 QV4-HT089
	7	17.8	84.8	634	6	CB082521	CB082521 hn52c01.g
c	8	17.8	84.8	702	5	BW403702	BW403702 BW403702